Please amend the claims as follows:

1. (Currently Amended) A reaction mixture, comprising:

a) a first oligonucleotide primer comprising i) a sequence corresponding to a T7 promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, ~~and~~ iv) a sequence coding for a first epitope marker, and v) a region of complementarity to a region of the APC gene; and

b) a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker, wherein said first and second epitope markers are selected from the group consisting of SEQ ID NOS: 5, 6, 7, 8 and 9, and wherein said first and second epitope markers are different.

2. (Currently Amended) The reaction mixture of Claim 1, further comprising:

c) template comprising a region of the APC gene.

3. (Cancelled)

4. (Original) The reaction mixture of Claim 2, wherein said second oligonucleotide primer further comprises iii) a region of complementarity to said template.

5. (Currently Amended) The reaction mixture of Claim 1 ~~3~~, wherein said region of complementarity is greater than 15 bases in length.

6. (Original) The reaction mixture of Claim 4, wherein said region of complementarity is greater than 15 bases in length.

7. (Cancelled)

8. (Cancelled)

9. (Currently Amended) A kit, comprising:

a) a first oligonucleotide primer comprising i) a sequence corresponding to a T7 promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, ~~and~~ iv) a sequence coding for a first epitope marker, and v) a region of complementarity to a region of the APC gene; and

b) a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker, wherein said first and second

epitope markers are selected from the group consisting of SEQ ID NOS: 5, 6, 7, 8 and 9, and wherein said first and second epitope markers are different.

10. (Cancelled)

11. (Original) The kit of Claim 9, wherein said second oligonucleotide primer further comprises iii) a region of complementarity to a template.

12. (Currently Amended) The kit of Claim 9 ~~10~~, wherein said region of complementarity is greater than 15 bases in length.

13. (Original) The kit of Claim 11, wherein said region of complementarity is greater than 15 bases in length.

14. (Cancelled)

15. (Cancelled)

16. (Currently Amended) A method of introducing coding sequence for epitope markers into nucleic acid, comprising:

a) providing:

i) the reaction mixture of Claim 2 ~~a first oligonucleotide primer comprising i) a sequence corresponding to a promoter, ii) a sequence corresponding to a ribosome binding site, iii) a start codon, and iv) a sequence coding for a first epitope marker~~;

ii) ~~a second oligonucleotide primer comprising i) at least one stop codon, and ii) a sequence encoding for a second epitope marker;~~

~~iii)~~ a polymerase; and

~~iv) template; and~~

b) mixing ~~said template with said first primer, second primer and~~ said polymerase and said reaction mixture under conditions such that amplified template is produced, said amplified template coding for said first and second epitope markers.

17. (Cancelled).

18. (Cancelled).

19. (Cancelled).

20. (Cancelled).

21. (Cancelled).

22. (Cancelled).

23. (Cancelled).

24. (Currently Amended) A method, comprising:
    a) providing:
        i) the amplified template of Claim 16 ~~22~~;
        ii) a misaminoacylated tRNA comprising an affinity marker; and
        iii) a translation system; and
    b) introducing said amplified template and said misaminoacylated tRNA into said translation system under conditions such that said affinity marker is incorporated into a nascent protein in a reaction mixture, whereby said nascent protein comprises 1) said first epitope marker, 2) said second epitope marker, and 3) said affinity marker.

25. (Original) The method of Claim 24, wherein said translation system is a cell-free translation system.

26. (Original) The method of Claim 25, wherein said cell-free translation system is selected from the group consisting of *Escherichia coli* lysates, wheat germ extracts, insect cell lysates, rabbit reticulocyte lysates, frog oocyte lysates, dog pancreatic lysates, human cell lysates, mixtures of purified or semi-purified translation factors and combinations thereof.

27. (Original) The method of Claim 24, wherein said affinity marker comprises a biotinyl moiety.

28. (Original) The method of Claim 24, wherein said misaminoacylated tRNA comprises BODIPY-FL-lysyl-tRNA.

29. (Original) The method of Claim 24, further comprising, after step b), step c) adding an antibody reactive with said second epitope marker.

30. (Cancelled).

31. (Withdrawn) A method, comprising:
    a) providing:
        i) the amplified template of Claim 23; and
        iii) a translation system;
    b) introducing said amplified template into said translation system under conditions such that a nascent protein is produced, said nascent protein comprising 1) said first epitope marker, 2) said second epitope marker, and 3) said affinity marker; and
    c) separating said nascent protein from said translation system using said affinity marker.

32. (Withdrawn) The method of Claim 31, wherein said translation system is a cell-free translation system.

33. (Withdrawn) The method of Claim 32, wherein said cell-free translation system is selected from the group consisting of *Escherichia coli* lysates, wheat germ extracts, insect cell lysates, rabbit reticulocyte lysates, frog oocyte lysates, dog pancreatic lysates, human cell lysates, mixtures of purified or semi-purified translation factors and combinations thereof.

34. (Withdrawn) The method of Claim 31, wherein said affinity marker comprises a third epitope marker.

35. (Withdrawn) The method of Claim 31, further comprising after step (c): d) analyzing for the presence of said first epitope marker and said second epitope marker.

36. (Withdrawn) The method of Claim 31, further comprising, after step (c): d) adding an antibody reactive with said second epitope marker.

37. (Withdrawn) The method of Claim 36, wherein said antibody is reactive with an epitope sequence selected from the group consisting of a HIS-tag, a C-myc-tag, a FLAG-tag, a STREP-tag, and an HA-tag.